AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A method of <u>diagnosing</u> ~~identifying individuals predisposed to~~ schizophrenia comprising:

  a) providing a nucleic acid from a human subject <u>suspected of having</u> <u>schizophrenia</u>; wherein said nucleic acid comprises an α7 allele;

  b) detecting ~~the presence of~~ at least one polymorphism within a core promoter region of said α7 allele, wherein said core promoter region corresponds to SEQ ID NO:125~~, and wherein said at least one polymorphism contributes to reduced transcription~~;

  c) <u>interviewing said subject by a physician, wherein said subject presents at</u> <u>least one symptom of schizophrenia;</u> ~~correlating the presence of said at least one polymorphism with a predisposition to schizophrenia:~~ and

  d) providing a diagnosis of schizophrenia to said subject based on the presence of said at least one polymorphism and <u>said at least one symptom,</u> <u>wherein said diagnosis differentiates schizophrenia from other forms of</u> <u>mental illness</u> ~~a physician interview~~.

2. (Previously Presented) The method of Claim 1, wherein said at least one polymorphism comprises a –86 C to T substitution in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125.

3-4. (Canceled)

5. (Original) The method of Claim 1, wherein said detecting step is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, denaturing high performance liquid chromatography, ligase chain reaction, comparative genome hybridisation, Southern blotting and sequencing.

6. (Original) The method of Claim 1, wherein said nucleic acid from said subject is derived from a sample selected from the group consisting of a biopsy material and blood.

7-25. (Canceled)

26. (Previously Presented) A method of identifying individuals predisposed to schizophrenia comprising:

    a)   providing a nucleic acid from a human subject; wherein said nucleic acid comprises an α7 allele; <u>and</u>

    b)   detecting ~~the presence of~~ at least one polymorphism within <u>SEQ ID NO:125 of</u> said α7 allele~~, wherein said at least one polymorphism comprises a -86 C to T substitution in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125~~; and

    c)   <u>identifying that said subject is predisposed to schizophrenia by said detected polymorphism</u> ~~correlating the presence of said at least one polymorphism with a predisposition to schizophrenia~~.

27-34. (Canceled)

35. (Previously Presented) The method of Claim 26, wherein said detecting step is accomplished using at least one technique selected from the group consisting of polymerase chain reaction, heteroduplex analysis, single stand conformational polymorphism analysis, denaturing high performance liquid chromatography, ligase chain reaction, comparative genome hybridisation, Southern blotting and sequencing.

36. (Previously Presented) The method of Claim 26, wherein said nucleic acid from said subject is derived from a sample selected from the group consisting of a biopsy material and blood.

37-38. (Canceled)

39. (New) The method of Claim 26, wherein said at least one polymorphism comprises a −86 C to T substitution in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125.

40. (New) The method of Claim 26, wherein said at least one polymorphism comprises a single variant in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125 selected from the group consisting of -86C/T; -92G/A, -143 G/A. −178 -G; -180 G/C; -191 G/A; -194 G/C; and -241 A/G.

41. (New) The method of Claim 26, wherein said at least one polymorphism comprises a dual variant in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO::125 selected from the group consisting of -46/-178; -146/-190; -46/-191; -86/-241; and -178/-191.

42. (New) The method of Claim 26, wherein the method further comprises, before step (c) determining a P50 test conditioning ratio.

43. (New) The method of Claim 42, wherein the method further comprises step (d) establishing that said subject is predisposed to schizophrenia by said detected polymorphism and said p50 test conditioning ratio of at least 0.5.

44. (New) The method of Claim 26, wherein said P50 test conditioning ratio is determined by an auditory hearing response test.

45. (New) The method of Claim 1, wherein said polymorphism comprises a single variant in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO:125 selected from the group consisting of -86C/T; -92G/A, -143 G/A. −178 -G; -180 G/C; -191 G/A; -194 G/C; and -241 A/G.

46. (New) The method of Claim 1, wherein said polymorphism comprises a dual variant in relation to a start codon of said α7 allele beginning at residue 270 of SEQ ID NO::125 selected from the group consisting of -46/-178; -146/-190; -46/-191; -86/-241; and -178/-191.